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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/071,223

DATE: 06/04/2002

TIME: 12:16:43

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Output Set: N:\CRF3\06042002\J071223.raw

ENTERED

4 <110> APPLICANT: Storm, Daniel R.
5 Hacker, Beth
6 Tomlinson, James E.
7 COR Therapeutics, Inc.
8 University of Washington
10 <120> TITLE OF INVENTION: CLONING AND CHARACTERIZATION OF A HUMAN ADENYLYL
11 CYCLASE
13 <130> FILE REFERENCE: 44481-5029-02-US
15 <140> CURRENT APPLICATION NUMBER: 10/071,223
16 <141> CURRENT FILING DATE: 2002-02-11
18 <150> PRIOR APPLICATION NUMBER: 09/473,717
19 <151> PRIOR FILING DATE: 1999-12-29
21 <150> PRIOR APPLICATION NUMBER: PCT/US98/13541
22 <151> PRIOR FILING DATE: 1998-07-01
24 <150> PRIOR APPLICATION NUMBER: 60/098,559
25 <151> PRIOR FILING DATE: 1997-07-01
27 <150> PRIOR APPLICATION NUMBER: 08/886,440
28 <151> PRIOR FILING DATE: 1997-07-01
30 <160> NUMBER OF SEQ ID NOS: 3
32 <170> SOFTWARE: PatentIn Ver. 2.0
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 4985
36 <212> TYPE: DNA
37 <213> ORGANISM: human type IX adenylyl cyclase
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48 cac agc acc gag gtg agc tgc gac tcc agc ggg gac agc aac agc gtg 100
49 His Ser Thr Glu Val Ser Cys Asp Ser Ser Gly Asp Ser Asn Ser Val
50 15 20 25
52 cgc gtc aag atc aac ccc aag cag ctg tcc tcc aac agc cac ccc aag 148
53 Arg Val Lys Ile Asn Pro Lys Gln Leu Ser Ser Asn Ser His Pro Lys
54 30 35 40
56 cac tgc aaa tac agc atc tcc tct agc tgc agc agc tct ggg gac tcc 196
57 His Cys Lys Tyr Ser Ile Ser Ser Ser Cys Ser Ser Ser Gly Asp Ser
58 45 50 55 60
60 ggg ggc gtc ccc cgg cga gtg ggc ggc gga ggc cgg ctg cgc agg cag 244
61 Gly Gly Val Pro Arg Arg Val Gly Gly Gly Gly Arg Leu Arg Arg Gln
62 65 70 75

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65 Lys Lys Leu Pro Gln Leu Phe Glu Arg Ala Ser Ser Arg Trp Trp Asp
66      80      85      90
68 ccc aag ttc gac tcg gtg aac ctg gag gag gcc tgc ctg gag cgc tgc 340
69 Pro Lys Phe Asp Ser Val Asn Leu Glu Glu Ala Cys Leu Glu Arg Cys
70      95      100      105
72 ttc ccg cag acc cag cgc cgg ttc cgg tat gcg ctc ttc tac atc ggc 388
73 Phe Pro Gln Thr Gln Arg Arg Phe Arg Tyr Ala Leu Phe Tyr Ile Gly
74      110      115      120
76 ttc gcc tgc ctt ctg tgg agc atc tat ttt gcg gtc cac atg aga tcc 436
77 Phe Ala Cys Leu Leu Trp Ser Ile Tyr Phe Ala Val His Met Arg Ser
78 125      130      135      140
80 aga ctg atc gtc atg gtc gcc ccc gcg ctg tgc ttc ctc ctg gtg tgt 484
81 Arg Leu Ile Val Met Val Ala Pro Ala Leu Cys Phe Leu Leu Val Cys
82      145      150      155
84 gtg ggc ttc ttt ctg ttt acc ttc acc aag ctg tac gcc cgg cat tac 532
85 Val Gly Phe Phe Leu Phe Thr Phe Thr Lys Leu Tyr Ala Arg His Tyr
86      160      165      170
88 gcg tgg acc tcg ctg gct ctc acc ctg ctg gtg ttc gcc ctg acc ctg 580
89 Ala Trp Thr Ser Leu Ala Leu Thr Leu Leu Val Phe Ala Leu Thr Leu
90      175      180      185
92 gct gcg cag ttc cag gtc ttg acg cct gtc tca gga cgc ggc gac agc 628
93 Ala Ala Gln Phe Gln Val Leu Thr Pro Val Ser Gly Arg Gly Asp Ser
94      190      195      200
96 tcc aac ctt acg gcc aca gcc cgg ccc aca gat act tgc tta tct caa 676
97 Ser Asn Leu Thr Ala Thr Ala Arg Pro Thr Asp Thr Cys Leu Ser Gln
98 205      210      215      220
100 gtg ggg agc ttc tcc atg tgc atc gaa gtg ctc ttt ttg ctc tat acc 724
101 Val Gly Ser Phe Ser Met Cys Ile Glu Val Leu Phe Leu Leu Tyr Thr
102      225      230      235
104 gtc atg cac tta cct ttg tac ctg agt ttg tgt ctg ggg gtg gcc tac 772
105 Val Met His Leu Pro Leu Tyr Leu Ser Leu Cys Leu Gly Val Ala Tyr
106      240      245      250
108 tct gtc ctt ttc gag acc ttt ggc tac cat ttc cgg gat gaa gcc tgc 820
109 Ser Val Leu Phe Glu Thr Phe Gly Tyr His Phe Arg Asp Glu Ala Cys
110      255      260      265
112 ttc ccc tcg ccc gga gcc ggg gcc ctg cac tgg gag ctg ctg agc agg 868
113 Phe Pro Ser Pro Gly Ala Gly Ala Leu His Trp Glu Leu Leu Ser Arg
114      270      275      280
116 ggg ctg ctc cac ggc tgc atc cac gcc atc ggg gtc cac ctg ttc gtc 916
117 Gly Leu Leu His Gly Cys Ile His Ala Ile Gly Val His Leu Phe Val
118 285      290      295      300
120 atg tcc cag gtg agg tcc agg agc acc ttc ctc aag gtg ggg caa tcc 964
121 Met Ser Gln Val Arg Ser Arg Ser Thr Phe Leu Lys Val Gly Gln Ser
122      305      310      315
124 att atg cac ggg aag gac ctg gaa gtg gaa aaa gcc ctc aaa gag agg 1012
125 Ile Met His Gly Lys Asp Leu Glu Val Glu Lys Ala Leu Lys Glu Arg
126      320      325      330
128 atg att cat tcc gtg atg cca aga atc ata gcc gat gac tta atg aag 1060

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133	Gln	Gly	Asp	Glu	Glu	Ser	Glu	Asn	Ser	Val	Lys	Arg	His	Ala	Thr	Ser	
134			350					355					360				
136	agc	ccc	aag	aac	agg	aag	aaa	aag	tct	tcc	atc	caa	aaa	gct	cct	ata	1156
137	Ser	Pro	Lys	Asn	Arg	Lys	Lys	Lys	Ser	Ser	Ile	Gln	Lys	Ala	Pro	Ile	
138	365						370				375					380	
140	gcc	ttc	cgc	cct	ttt	aag	atg	cag	cag	atc	gaa	gaa	gtc	agt	att	tta	1204
141	Ala	Phe	Arg	Pro	Phe	Lys	Met	Gln	Gln	Ile	Glu	Glu	Val	Ser	Ile	Leu	
142						385					390				395		
144	ttt	gca	gat	atc	gtg	ggc	ttc	acc	aag	atg	agt	gcc	aac	aag	tct	gcc	1252
145	Phe	Ala	Asp	Ile	Val	Gly	Phe	Thr	Lys	Met	Ser	Ala	Asn	Lys	Ser	Ala	
146				400					405					410			
148	cac	gcc	ctg	gtg	ggg	ctc	ctg	aac	gat	ctg	ttc	ggg	cgc	ttc	gac	cgc	1300
149	His	Ala	Leu	Val	Gly	Leu	Leu	Asn	Asp	Leu	Phe	Gly	Arg	Phe	Asp	Arg	
150			415					420					425				
152	ctg	tgt	gag	gag	acc	aag	tgt	gag	aaa	atc	agc	acc	ctg	gga	gac	tgt	1348
153	Leu	Cys	Glu	Glu	Thr	Lys	Cys	Glu	Lys	Ile	Ser	Thr	Leu	Gly	Asp	Cys	
154			430					435					440				
156	tac	tac	tgc	gtg	gcg	ggc	tgt	ccc	gag	ccc	cgg	gcc	gac	cat	gcc	tac	1396
157	Tyr	Tyr	Cys	Val	Ala	Gly	Cys	Pro	Glu	Pro	Arg	Ala	Asp	His	Ala	Tyr	
158	445					450					455					460	
160	tgc	tgc	atc	gag	atg	ggc	ctg	ggc	atg	atc	aag	gcc	atc	gag	cag	ttc	1444
161	Cys	Cys	Ile	Glu	Met	Gly	Leu	Gly	Met	Ile	Lys	Ala	Ile	Glu	Gln	Phe	
162					465				470						475		
164	tgc	cag	gag	aag	aag	gag	atg	gtg	aac	atg	aga	gtc	ggg	gtg	cac	acg	1492
165	Cys	Gln	Glu	Lys	Lys	Glu	Met	Val	Asn	Met	Arg	Val	Gly	Val	His	Thr	
166				480					485					490			
168	ggc	acc	gtc	ctt	tgc	ggc	atc	ctg	ggc	atg	agg	agg	ttt	aaa	ttt	gac	1540
169	Gly	Thr	Val	Leu	Cys	Gly	Ile	Leu	Gly	Met	Arg	Arg	Phe	Lys	Phe	Asp	
170			495					500					505				
172	gtg	tgg	tcc	aac	gat	gtg	aac	ctg	gcc	aat	ctc	atg	gag	cag	ctg	gga	1588
173	Val	Trp	Ser	Asn	Asp	Val	Asn	Leu	Ala	Asn	Leu	Met	Glu	Gln	Leu	Gly	
174			510					515					520				
176	gtg	gcc	ggc	aaa	gtt	cac	att	tct	gag	gcc	acc	gca	aaa	tac	tta	gat	1636
177	Val	Ala	Gly	Lys	Val	His	Ile	Ser	Glu	Ala	Thr	Ala	Lys	Tyr	Leu	Asp	
178	525					530					535					540	
180	gac	cgg	tac	gaa	atg	gaa	gat	ggg	aaa	gtt	att	gaa	cgg	ctg	ggc	cag	1684
181	Asp	Arg	Tyr	Glu	Met	Glu	Asp	Gly	Lys	Val	Ile	Glu	Arg	Leu	Gly	Gln	
182				545					550						555		
184	agc	gtg	gtt	gct	gac	cag	ttg	aaa	ggg	ttg	aag	aca	tac	ctg	ata	tcg	1732
185	Ser	Val	Val	Ala	Asp	Gln	Leu	Lys	Gly	Leu	Lys	Thr	Tyr	Leu	Ile	Ser	
186				560					565					570			
188	ggg	cag	aga	gcc	aag	gag	tct	cgc	tgc	agc	tgt	gca	gag	gcc	ttg	ctt	1780
189	Gly	Gln	Arg	Ala	Lys	Glu	Ser	Arg	Cys	Ser	Cys	Ala	Glu	Ala	Leu	Leu	
190			575					580					585				
192	tct	ggc	ttt	gag	gtc	att	gac	ggc	tca	cag	gtg	tcc	tca	ggc	cct	agg	1828
193	Ser	Gly	Phe	Glu	Val	Ile	Asp	Gly	Ser	Gln	Val	Ser	Ser	Gly	Pro	Arg	

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196 gga cag ggg aca gcg tca tca ggg aat gtc agt gac ttg gcg cag act 1876
197 Gly Gln Gly Thr Ala Ser Ser Gly Asn Val Ser Asp Leu Ala Gln Thr
198 605      610      615      620
200 gtc aaa acc ttt gat aac ctt aag acc tgc cct tcg tgc gga atc aca 1924
201 Val Lys Thr Phe Asp Asn Leu Lys Thr Cys Pro Ser Cys Gly Ile Thr
202      625      630      635
204 ttt gct ccc aaa tct gaa gcc ggc gcc gag gga gga gca cct caa aac 1972
205 Phe Ala Pro Lys Ser Glu Ala Gly Ala Glu Gly Gly Ala Pro Gln Asn
206      640      645      650
208 ggc tgc caa gac gag cat aaa aac agc acc aag gct tct gga gga cct 2020
209 Gly Cys Gln Asp Glu His Lys Asn Ser Thr Lys Ala Ser Gly Gly Pro
210      655      660      665
212 aat ccc aaa act cag aac ggg ctc ctc agc cct ccc caa gag gag aag 2068
213 Asn Pro Lys Thr Gln Asn Gly Leu Leu Ser Pro Pro Gln Glu Glu Lys
214      670      675      680
216 ctc acc aac agt cag act tct ctg tgt gag atc ttg cag gag aag gga 2116
217 Leu Thr Asn Ser Gln Thr Ser Leu Cys Glu Ile Leu Gln Glu Lys Gly
218 685      690      695      700
220 agg tgg gca ggg gtg agc ctg gac cag tcg gct ctc ctt ccg ctg agg 2164
221 Arg Trp Ala Gly Val Ser Leu Asp Gln Ser Ala Leu Leu Pro Leu Arg
222      705      710      715
224 ttc aag aac atc cgg gag aaa acg gac gcc cac ttt gtg gac gtt atc 2212
225 Phe Lys Asn Ile Arg Glu Lys Thr Asp Ala His Phe Val Asp Val Ile
226      720      725      730
228 aaa gaa gac agc ctg atg aaa gat tac ttt ttt aag ccg ccc att aat 2260
229 Lys Glu Asp Ser Leu Met Lys Asp Tyr Phe Phe Lys Pro Pro Ile Asn
230      735      740      745
232 cag ttc agc ctg aac ttc ctg gat cag gag ctg gag cga tcc tac agg 2308
233 Gln Phe Ser Leu Asn Phe Leu Asp Gln Glu Leu Glu Arg Ser Tyr Arg
234      750      755      760
236 acc agc tat cag gaa gag gtc ata aag aac tcc ccc gtg aag acg ttt 2356
237 Thr Ser Tyr Gln Glu Glu Val Ile Lys Asn Ser Pro Val Lys Thr Phe
238 765      770      775      780
240 gct agt ccc acc ttc agc tcc ctc ctg gat gtg ttt ctg tcg acc aca 2404
241 Ala Ser Pro Thr Phe Ser Ser Leu Leu Asp Val Phe Leu Ser Thr Thr
242      785      790      795
244 gtg ttt ctg acg ctg tcc acc acc tgc ttc ctg aag tac gag gcg gcc 2452
245 Val Phe Leu Thr Leu Ser Thr Thr Cys Phe Leu Lys Tyr Glu Ala Ala
246      800      805      810
248 acc gtg cct ccc ccg ccc gcc gcc ctg gcg gtc ttc agt gca gcc ctg 2500
249 Thr Val Pro Pro Pro Pro Ala Ala Leu Ala Val Phe Ser Ala Ala Leu
250      815      820      825
252 ctg ctg gag gtg ctg tcc ctc gcg gtg tcc atc agg atg gtg ttc ttc 2548
253 Leu Leu Glu Val Leu Ser Leu Ala Val Ser Ile Arg Met Val Phe Phe
254      830      835      840
256 ctg gag gac gtc atg gcc tgc acc aag cgc ctg ctg gag tgg atc gcc 2596
257 Leu Glu Asp Val Met Ala Cys Thr Lys Arg Leu Leu Glu Trp Ile Ala
258 845      850      855      860

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260	ggc	tgg	cta	cca	cgt	cac	tgc	atc	ggg	gcc	atc	ctg	gtg	tcg	ctt	ccc	2644
261	Gly	Trp	Leu	Pro	Arg	His	Cys	Ile	Gly	Ala	Ile	Leu	Val	Ser	Leu	Pro	
262					865					870					875		
264	gca	ctg	gcc	gtc	tac	tcc	cat	gtc	acc	tcc	gaa	tat	gag	acc	aac	ata	2692
265	Ala	Leu	Ala	Val	Tyr	Ser	His	Val	Thr	Ser	Glu	Tyr	Glu	Thr	Asn	Ile	
266					880					885					890		
268	cac	ttc	cca	gtg	ttc	aca	ggc	tcg	gcc	gca	ctg	att	gcc	gtc	gtg	cac	2740
269	His	Phe	Pro	Val	Phe	Thr	Gly	Ser	Ala	Ala	Leu	Ile	Ala	Val	Val	His	
270					895					900					905		
272	tac	tgt	aac	ttc	tgc	cag	ctc	agc	tcc	tgg	atg	agg	tcc	tcc	ctc	gcc	2788
273	Tyr	Cys	Asn	Phe	Cys	Gln	Leu	Ser	Ser	Trp	Met	Arg	Ser	Ser	Leu	Ala	
274					910					915					920		
276	acc	gtc	gtg	ggg	gcc	ggg	ccg	ctg	ctc	ctg	ctc	tac	gtc	tcc	ctg	tgc	2836
277	Thr	Val	Val	Gly	Ala	Gly	Pro	Leu	Leu	Leu	Leu	Tyr	Val	Ser	Leu	Cys	
278	925						930					935				940	
280	cca	gac	agt	tct	gta	tta	act	tcg	ccc	ctt	gac	gca	gta	cag	aat	ttc	2884
281	Pro	Asp	Ser	Ser	Val	Leu	Thr	Ser	Pro	Leu	Asp	Ala	Val	Gln	Asn	Phe	
282					945					950					955		
284	agt	tcc	gag	agg	aac	ccg	tgc	aat	agt	tcg	gtg	ccg	cgt	gac	ctc	cgg	2932
285	Ser	Ser	Glu	Arg	Asn	Pro	Cys	Asn	Ser	Ser	Val	Pro	Arg	Asp	Leu	Arg	
286					960					965					970		
288	cgg	ccc	gcc	agc	ctc	atc	ggc	cag	gag	gtg	gtt	ctc	gtc	ttc	ttt	ctc	2980
289	Arg	Pro	Ala	Ser	Leu	Ile	Gly	Gln	Glu	Val	Val	Leu	Val	Phe	Phe	Leu	
290					975					980					985		
292	ctg	ctc	ttg	ttg	gtc	tgg	ttc	ctg	aat	cgc	gaa	ttt	gaa	gtc	agc	tac	3028
293	Leu	Leu	Leu	Leu	Val	Trp	Phe	Leu	Asn	Arg	Glu	Phe	Glu	Val	Ser	Tyr	
294					990					995					1000		
296	cgc	ctc	cac	tac	cac	gga	gac	gtg	gaa	gcg	gat	ctt	cac	cgc	acc	aag	3076
297	Arg	Leu	His	Tyr	His	Gly	Asp	Val	Glu	Ala	Asp	Leu	His	Arg	Thr	Lys	
298	1005					1010					1015				1020		
300	atc	cag	agc	atg	cgg	gac	cag	gca	gac	tgg	ctg	ctg	agg	aac	atc	atc	3124
301	ile	Gln	Ser	Met	Arg	Asp	Gln	Ala	Asp	Trp	Leu	Leu	Arg	Asn	Ile	Ile	
302					1025					1030					1035		
304	ccc	tac	cac	gtg	gct	gag	cag	ctg	aag	gtg	tcc	cag	acc	tac	tcc	aag	3172
305	Pro	Tyr	His	Val	Ala	Glu	Gln	Leu	Lys	Val	Ser	Gln	Thr	Tyr	Ser	Lys	
306					1040					1045					1050		
308	aac	cac	gac	agc	gga	ggg	gtg	atc	ttc	gcc	agc	atc	gtc	aac	ttc	agc	3220
309	Asn	His	Asp	Ser	Gly	Gly	Val	Ile	Phe	Ala	Ser	Ile	Val	Asn	Phe	Ser	
310					1055					1060					1065		
312	gag	ttc	tac	gag	gag	aac	tac	gag	ggc	ggc	aag	gag	tgc	tac	cgg	gtc	3268
313	Glu	Phe	Tyr	Glu	Glu	Asn	Tyr	Glu	Gly	Gly	Lys	Glu	Cys	Tyr	Arg	Val	
314					1070					1075					1080		
316	ctc	aac	gag	ctc	atc	ggg	gac	ttt	gac	gag	ctc	cta	agc	aag	ccg	gac	3316
317	Leu	Asn	Glu	Leu	Ile	Gly	Asp	Phe	Asp	Glu	Leu	Leu	Ser	Lys	Pro	Asp	
318	1085					1090					1095				1100		
320	tac	agc	agc	atc	gag	aag	atc	aag	acc	atc	gga	gcc	acg	tac	atg	gcg	3364
321	Tyr	Ser	Ser	Ile	Glu	Lys	Ile	Lys	Thr	Ile	Gly	Ala	Thr	Tyr	Met	Ala	
322					1105					1110					1115		
324	gcg	tca	ggg	ctg	aac	acc	gcg	cag	gcc	cag	gac	ggc	agc	cac	ccg	cag	3412

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